

RAW SEQUENCE LISTING

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Application Serial Number: 10|806477
Source: IFWO
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RAW SEQUENCE LISTING

DATE: 10/14/2005

PATENT APPLICATION: US/10/806,477

TIME: 09:39:23

Input Set : N:\Cr3\RULE60\10806477.raw

Output Set: N:\CRF4\10142005\J806477.raw

SEQUENCE LISTING

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1 (1) GENERAL INFORMATION:
2   (i) APPLICANT: Engler, Jeffrey A
3           Lee, Jae Hwy
4           Collawan, James F
5           Moore, Bryan A
6   (ii) TITLE OF INVENTION: Receptor-Mediated Uptake of Peptides
7           that Bind the Human Transferrin Receptor
8   (iii) NUMBER OF SEQUENCES: 14
9   (iv) CORRESPONDENCE ADDRESS:
10          (A) ADDRESSEE: Hendricks and Assoc.
11          (B) STREET: P.O. Box 2509
12          (C) CITY: Fairfax
13          (D) STATE: VA
14          (E) COUNTRY: U.S.A
15          (F) ZIP: 22031
16   (v) COMPUTER READABLE FORM:
17          (A) MEDIUM TYPE: Floppy disk
18          (B) COMPUTER: IBM PC compatible
19          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
20          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
21   (vi) CURRENT APPLICATION DATA:
C--> 22          (A) APPLICATION NUMBER: US/10/806,477
C--> 23          (B) FILING DATE: 23-Mar-2004
W--> 28          (C) CLASSIFICATION:
C--> 25   (vii) PRIOR APPLICATION DATA:
26          (A) APPLICATION NUMBER: US/09/995,804
27          (B) FILING DATE: 29-Nov-2001
29   (viii) ATTORNEY/AGENT INFORMATION:
30          (A) NAME: Hendricks, Glenna M
31          (B) REGISTRATION NUMBER: 32,535
32          (C) REFERENCE/DOCKET NUMBER: engler1
33   (ix) TELECOMMUNICATION INFORMATION:
34          (A) TELEPHONE: 703/425-8405
35          (B) TELEFAX: 703/425-8406
36 (2) INFORMATION FOR SEQ ID NO: 1:
37   (i) SEQUENCE CHARACTERISTICS:
38          (A) LENGTH: 7 amino acids
39          (B) TYPE: amino acid
40          (C) STRANDEDNESS: single
41          (D) TOPOLOGY: unknown
42   (ii) MOLECULE TYPE: peptide
43   (iii) HYPOTHETICAL: NO

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44      (iv) ANTI-SENSE: NO
45      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
46          His Ala Ile Tyr Pro Arg His
47              1           5
49 (2) INFORMATION FOR SEQ ID NO: 2:
50      (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 12 amino acids
52          (B) TYPE: amino acid
53          (C) STRANDEDNESS: single
54          (D) TOPOLOGY: unknown
55      (ii) MOLECULE TYPE: peptide
56      (iii) HYPOTHETICAL: NO
57      (iv) ANTI-SENSE: NO
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
59          Thr His Arg Pro Pro Met Trp Ser Pro Val Trp Pro
60              1           5               10
62 (2) INFORMATION FOR SEQ ID NO: 3:
63      (i) SEQUENCE CHARACTERISTICS:
64          (A) LENGTH: 7 amino acids
65          (B) TYPE: amino acid
66          (C) STRANDEDNESS: single
67          (D) TOPOLOGY: unknown
68      (ii) MOLECULE TYPE: peptide
69      (iii) HYPOTHETICAL: NO
70      (iv) ANTI-SENSE: NO
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
72          Ile Arg His Pro His Tyr Ala
73              1           5
75 (2) INFORMATION FOR SEQ ID NO: 4:
76      (i) SEQUENCE CHARACTERISTICS:
77          (A) LENGTH: 12 amino acids
78          (B) TYPE: amino acid
79          (C) STRANDEDNESS: single
80          (D) TOPOLOGY: unknown
81      (ii) MOLECULE TYPE: peptide
82      (iii) HYPOTHETICAL: NO
83      (iv) ANTI-SENSE: NO
84      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
85          Pro Trp Arg Pro Ser His Pro Val Trp Met Pro Thr
86              1           5               10
88 (2) INFORMATION FOR SEQ ID NO: 5:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 18 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: unknown
94      (ii) MOLECULE TYPE: DNA (genomic)
95      (iii) HYPOTHETICAL: NO
96      (iv) ANTI-SENSE: NO

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97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
98      TGGGATTTTG CTAAAAAC
100 (2) INFORMATION FOR SEQ ID NO: 6:
101      (i) SEQUENCE CHARACTERISTICS:
102          (A) LENGTH: 22 base pairs
103          (B) TYPE: nucleic acid
104          (C) STRANDEDNESS: single
105          (D) TOPOLOGY: unknown
106      (ii) MOLECULE TYPE: DNA (genomic)
107      (iii) HYPOTHETICAL: NO
108      (iv) ANTI-SENSE: NO
109      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
110      GTATGGGATT TTGCTAAACA AC
112 (2) INFORMATION FOR SEQ ID NO: 7:
113      (i) SEQUENCE CHARACTERISTICS:
114          (A) LENGTH: 28 base pairs
115          (B) TYPE: nucleic acid
116          (C) STRANDEDNESS: single
117          (D) TOPOLOGY: unknown
118      (ii) MOLECULE TYPE: DNA (genomic)
119      (iii) HYPOTHETICAL: NO
120      (iv) ANTI-SENSE: NO
121      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
122      TCTAGATCTG ATGAGTAAAG GAGAAGAA
124 (2) INFORMATION FOR SEQ ID NO: 8:
125      (i) SEQUENCE CHARACTERISTICS:
126          (A) LENGTH: 54 base pairs
127          (B) TYPE: nucleic acid
128          (C) STRANDEDNESS: single
129          (D) TOPOLOGY: unknown
130      (ii) MOLECULE TYPE: DNA (genomic)
131      (iii) HYPOTHETICAL: NO
132      (iv) ANTI-SENSE: NO
133      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
134      TTAAAGCTTT TAATGGCGCG GATAGATCGC ATGTTTGTAG AGCTCATCCA TGCC
136 (2) INFORMATION FOR SEQ ID NO: 9:
137      (i) SEQUENCE CHARACTERISTICS:
138          (A) LENGTH: 68 base pairs
139          (B) TYPE: nucleic acid
140          (C) STRANDEDNESS: single
141          (D) TOPOLOGY: unknown
142      (ii) MOLECULE TYPE: DNA (genomic)
143      (iii) HYPOTHETICAL: NO
144      (iv) ANTI-SENSE: NO
145      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
146      TAAAGCTTTT ACGGCCACAC CGGGCTCCAC ATCGGCGGGC GGTGGGTTTT GTAGAGCTCA
147      TCCATGCC
149 (2) INFORMATION FOR SEQ ID NO: 10:
150      (i) SEQUENCE CHARACTERISTICS:

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151      (A) LENGTH: 29 base pairs
152      (B) TYPE: nucleic acid
153      (C) STRANDEDNESS: single
154      (D) TOPOLOGY: unknown
155      (ii) MOLECULE TYPE: DNA (genomic)
156      (iii) HYPOTHETICAL: NO
157      (iv) ANTI-SENSE: NO
158      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
159      GATCCCATGC GATCTATCCG CGCCATTAA                                29
161 (2) INFORMATION FOR SEQ ID NO: 11:
162      (i) SEQUENCE CHARACTERISTICS:
163          (A) LENGTH: 29 base pairs
164          (B) TYPE: nucleic acid
165          (C) STRANDEDNESS: single
166          (D) TOPOLOGY: unknown
167      (ii) MOLECULE TYPE: DNA (genomic)
168      (iii) HYPOTHETICAL: NO
169      (iv) ANTI-SENSE: YES
170      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
171      GATCTTAATG GCGCGGATAG ATCGCATGG                                29
173 (2) INFORMATION FOR SEQ ID NO: 12:
174      (i) SEQUENCE CHARACTERISTICS:
175          (A) LENGTH: 44 base pairs
176          (B) TYPE: nucleic acid
177          (C) STRANDEDNESS: single
178          (D) TOPOLOGY: unknown
179      (ii) MOLECULE TYPE: DNA (genomic)
180      (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
182      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
183      GATCCACCCA CCGCCCGCCG ATGTGGAGCC CGGTGTGGCC GTAA            44
185 (2) INFORMATION FOR SEQ ID NO: 13:
186      (i) SEQUENCE CHARACTERISTICS:
187          (A) LENGTH: 44 base pairs
188          (B) TYPE: nucleic acid
189          (C) STRANDEDNESS: single
190          (D) TOPOLOGY: unknown
191      (ii) MOLECULE TYPE: DNA (genomic)
192      (iii) HYPOTHETICAL: NO
193      (iv) ANTI-SENSE: YES
194      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
195      GATCTTACGG CCACACCGGG CTCCACATCG GCGGGCGGGT GGTG            44
197 (2) INFORMATION FOR SEQ ID NO: 14:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 7 amino acids
200          (B) TYPE: amino acid
201          (C) STRANDEDNESS: single
202          (D) TOPOLOGY: unknown
203      (ii) MOLECULE TYPE: peptide

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204 (iii) HYPOTHETICAL: NO
205 (iv) ANTI-SENSE: NO
206 (v) FRAGMENT TYPE: internal
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
208 His Ala Ile Tyr Pro Asn His
209 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/806,477

DATE: 10/14/2005

TIME: 09:39:24

Input Set : N:\Crf3\RULE60\10806477.raw

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:25 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:28 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)